

# Using DNA metabarcoding to identify the bacteria composition in water at *Kappaphycus alvarezii* cultivation sites infected by ice-ice from Labuhan Sangoro, Sumbawa, Indonesia

<sup>1</sup>Baiq H. Astriana, <sup>1</sup>Edwin Jefri, <sup>1</sup>Mahardika R. Himawan, <sup>2</sup>Lutfi Anggadhania, <sup>3</sup>Aryan P. Putra, <sup>4</sup>Baiq F. Arlina

<sup>1</sup> Marine Science Study Program, Faculty of Agriculture, University of Mataram, Mataram, West Nusa Tenggara, Indonesia; <sup>2</sup> Research Center for Applied Microbiology, National Research and Innovation Agency (BRIN), Soekarno Science Center, Cibinong, Bogor, West Java, Indonesia; <sup>3</sup> Master Program in Environmental Science, Muhammadiyah University of Mataram, Mataram, West Nusa Tenggara, Indonesia; <sup>4</sup> Environmental Science Study Program, Faculty of Mathematics and Natural Sciences, University of Mataram, Gomong, Selaparang, Mataram, West Nusa Tenggara, Indonesia. Corresponding author: B. H. Astriana, hilda.baiq@unram.ac.id

**Abstract.** Labuhan Sangoro, located in Saleh Bay, Sumbawa Regency, West Nusa Tenggara, Indonesia, is one of the areas developed for cultivation of seaweed species *Kappaphycus alvarezii*. In 2023, the cultivation activities experienced crop failure due to an outbreak of ice-ice disease. This incident has caused significant labor and financial losses for the farmers. It is suspected that biological factors (bacteria) play a role in the emergence of this disease. Therefore, this study aimed (1) to identify the bacteria living in the waters (ice-ice-infected seaweed cultivation site) and (2) to find potential bacterial species responsible for causing the ice-ice disease. The target of this research was to molecularly identify the potential bacterial species known to infect *K. alvarezii*, causing the disease. The method used in this research was exploratory descriptive. Samples were collected from 4 points (*K. alvarezii* cultivation locations infected by ice-ice). Each point was represented by 2 depths (surface and bottom waters). Samples analysis employed a culture-independent approach using metabarcoding (eDNA) analysis. This approach can be used to examine the genomes available in the environmental samples, thus allowing the identification of a wider range of bacterial species. As such, this approach offers greater opportunities to discover potential bacterial species that cause the ice-ice disease. In this research, the bacterial composition at two depths (surface and bottom waters) has been comprehensively understood. The major phyla responsible for important roles in organic matter decomposition, nutrient recycling, supporting primary production, and maintaining ecosystem balance are Cyanobacteria and Proteobacteria. The ice-ice disease in *K. alvarezii* culture is associated with certain bacterial species such as *Vibrio* spp. and *Pseudoalteromonas* sp. also found in the sampling locations.

**Key Words:** environmental DNA, ice-ice disease, *K. alvarezii*, marine bacteria, Saleh Bay.

**Introduction.** *Kappaphycus alvarezii* has become one of the Indonesian leading products, with national production reaching 8.3 million tons in 2013, the first rank in global production (Asaf et al 2021). In West Nusa Tenggara (NTB), the development of *K. alvarezii* cultivation is focused on several areas, one of which is Saleh Bay area in Sumbawa Regency. The selection of this area is based on its potential to provide environmental services along with the ecological resources it possesses (Yulius et al 2017). The growth of *Kappaphycus alvarezii*, a type of red algae known for its carrageenan content (Rupert et al 2022), has a notable obstacle in the form of ice-ice disease. Initially documented in the Philippines in 1974, this ailment has

subsequently emerged as a significant impediment in the cultivation of seaweed, resulting in extensive reductions in production and adversely impacting the economic well-being of coastal communities (Santoso & Nugraha 2008; Arasamuthu & Edward 2018; Aris et al 2020). Ice-ice is a disease caused by opportunistic pathogens that usually attack when environmental conditions are not optimal for seaweed survival (Riyaz et al 2019). The disease is distinguished by the presence of white and tender sections on the affected seaweed, indicating a significant disturbance in its typical structure and function (Arisandi & Farid 2014; Aris & Labenua 2020). In NTB, ice-ice outbreak was experienced by *K. alvarezii* cultivations in the waters of Labuhan Sangoro, Saleh Bay, Sumbawa Regency. This occurred in early 2023 and resulted in significant labor and financial losses for the farmers, most of whom rely on this activity for their livelihood (Astriana et al 2023).

Both abiotic and biotic variables influence the occurrence of ice-ice infection (Tahiluddin & Terzi 2021; Azis et al 2022). Unfavorable climatic circumstances such as excessive temperature, irradiance, and salinity can promote the disease (Erbabley & Kelabora 2018; Tahiluddin & Terzi 2021). Additionally, opportunistic bacterial pathogens play a vital part in the infection process (Azis et al 2022). Understanding the bacterial composition of affected areas on ice-ice disease is critical for creating efficient disease management techniques.

Traditional methods of identifying bacterial pathogens frequently rely on cultivation procedures, which can be time-consuming and may fail to capture the full diversity of the microbial population (Afianti & Darmayati 2019). Molecular approach that is currently widely used is environmental DNA (eDNA) metabarcoding. Environmental DNA refers to the DNA of an organism and extra-organismal DNA originating from marine, terrestrial, and aerial environments, such as water and sediment samples (Pranata et al 2022). DNA metabarcoding, a high-throughput sequencing approach, is an effective tool for evaluating numerous DNA sequences from complex microbial communities at the same time (Abdelfattah et al 2018). This method enables the identification and quantification of diverse bacterial species found in seaweed samples, offering a thorough understanding of the microbial dynamics involved in ice-ice disease.

Recent research has isolated a wide variety of seaweed-associated bacteria from *K. alvarezii*, including species from the genera *Alteromonas*, *Aestuariibacter*, *Idiomarina*, *Jejuia*, *Halomonas*, *Primorskyibacter*, *Pseudoalteromonas*, *Ruegeria*, *Terasakiella*, and *Vibrio* (Azizi et al 2018). These bacteria can cling to the seaweed surface and induce infection, resulting in a considerable drop in seaweed production and quality. Certain bacterial strains, such as *Vibrio alginolyticus* strain ABI-TU15, have been related to agarolytic activity and pathogenic potential (Azizi et al 2018).

The molecular characterisation of bacteria causing ice-ice disease found that the isolated bacteria are closely related to the genera *Vibrio*, *Pasteurella*, *Edwardsiella*, *Plesiomonas*, *Chromobacterium* (Azis et al 2022), *Alteromonas*, *Pseudoalteromonas*, and *Aurantimonas* (Kane et al 2016). These findings emphasize the necessity of understanding the genetic variety of the causal organisms in ice-ice illness in order to create tailored treatments. The purpose of this study is to use DNA metabarcoding to determine the bacterium composition at ice-ice infected *K. alvarezii* seaweed aquaculture sites. Using this advanced technique to analyze bacterial communities, we can get insight into the complex interactions between seaweed and its microbial environment. This understanding will help build more effective disease management techniques, as well as improve the general health and production of *K. alvarezii* farms.

## Material and Method

**Sampling.** The study was carried out in the Labuhan Sangoro Sea waters, namely in the Saleh Bay area of Sumbawa Regency, from May to October 2024. The sampling was conducted using a purposive approach, specifically targeting places where seaweed agricultural activities take place. Four samples were collected from specific places where *K. alvarezii* seaweed cultivation

was affected by ice-ice. Samples of seawater from two specific depths were collected: the surface (where the seaweed is grown at a depth of around 30-50 cm), and the near-bottom region of the water.

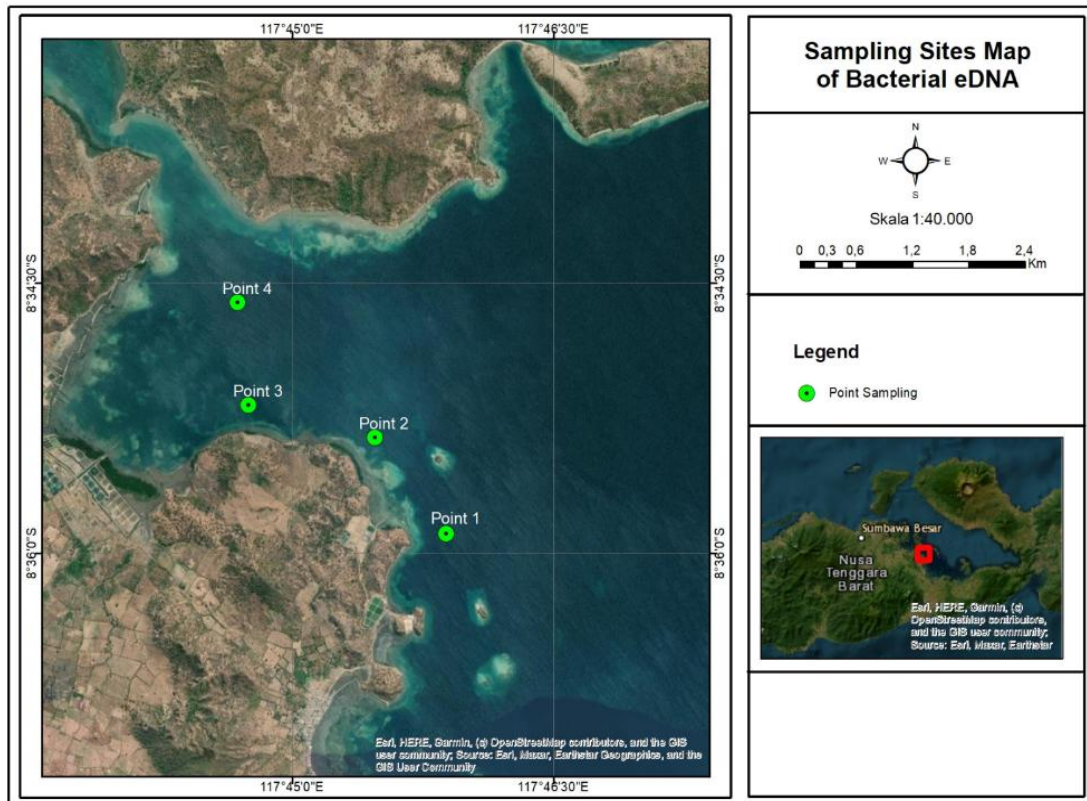


Figure 1. Sampling points at Labuhan Sangoro, Saleh Bay, Sumbawa Regency, West Nusa Tenggara.

**Genomic material isolation.** The DNA extraction from the samples was performed using the Qiagen Blood and Tissue DNA Extraction Kit, following the instructions provided by the manufacturer. The initial polymerase chain reaction (PCR) was performed to amplify the specific area of the 16S gene using 341F-518R primers, as described by Zhou et al (2017). The initial PCR reaction consisted of 10  $\mu$ L of Phanta Flash Master Mix (2x), 1  $\mu$ L of each 10 nM primer (F and R), 11  $\mu$ L of ddH<sub>2</sub>O, and 2  $\mu$ L of DNA template. The DNA amplification PCR profile consisted of the following phases. The process involves several steps: (1) heating the template DNA at 95°C for 5 min to prepare it for denaturation; (2) denaturing the template DNA at 98°C for 30 seconds; (3) annealing at 67°C for 30 seconds; (4) extending the DNA at 72°C for 30 seconds; and (5) performing a final extension at 72°C for 5 min. These steps are repeated for 35 cycles, starting from step (2) and ending with step (4). The 96 Universal peqSTAR PCR machine was utilized to detect any presence of contamination, employing negative controls in the form of a blank template. The PCR product quality was assessed by seeing it through electrophoresis on a 2% agarose gel, prepared with 100 mL of TAE buffer and 1 g of agarose. A 2  $\mu$ L portion of the PCR result was subsequently placed into each agarose well along with a 100 bp DNA ladder in one of the wells. The electrophoresis machine was run at 100 volts for 30 min, and the results were seen using UV fluorescence via an Alpha Imager Mini Gel Documentation System.

For indexing purposes, all triplicate PCR results that passed the electrophoresis quality control underwent a second PCR. The IDT double index and Illumina sequencing adaptor for

Illumina Nextera DNA Unique Dual Index, Set B were added to the target amplicon in the second PCR. The PCR cycle comprised an initial denaturation at 95°C (3 min), then 9 cycles of 95°C for 30 seconds, 55°C for 30 seconds, 72°C for 30 seconds, and a final extension at 72°C for 5 min. PCR purification was undertaken on the first PCR and second PCR products using AMPure XP before proceeding to the next stage. The amplicon library was quantified using a Qubit fluorometer, then normalized at equal concentration. DNA sequencing was performed on a NovaSEQ6000.

**Taxonomic classification.** The datasets were demultiplexed into FASTQ files and then imported into Quantitative Insights into Microbial Ecology (QIIME2; v2024.5). The raw sequence reads were quality-checked using the “qiime demux summarize” function and denoised using DADA2 (q2-dada2 denoise-paired) (Callahan et al 2016). The “q2-feature-table tabulate-seqs” command was used to generate representative sequences (rep-seqs). Taxonomic identifications (ids) represented the respective sequences assigned to ASVs against the Silva-138-99-nb-classifier (Yilmaz et al 2014).

**Results.** The taxonomic analysis revealed a diverse range of bacterial phyla across both sites. The most abundant phylum at both locations was Cyanobacteria, with class Oxyphotobacteria, followed by Proteobacteria, with class Alphaproteobacteria (Figures 2 and 3).

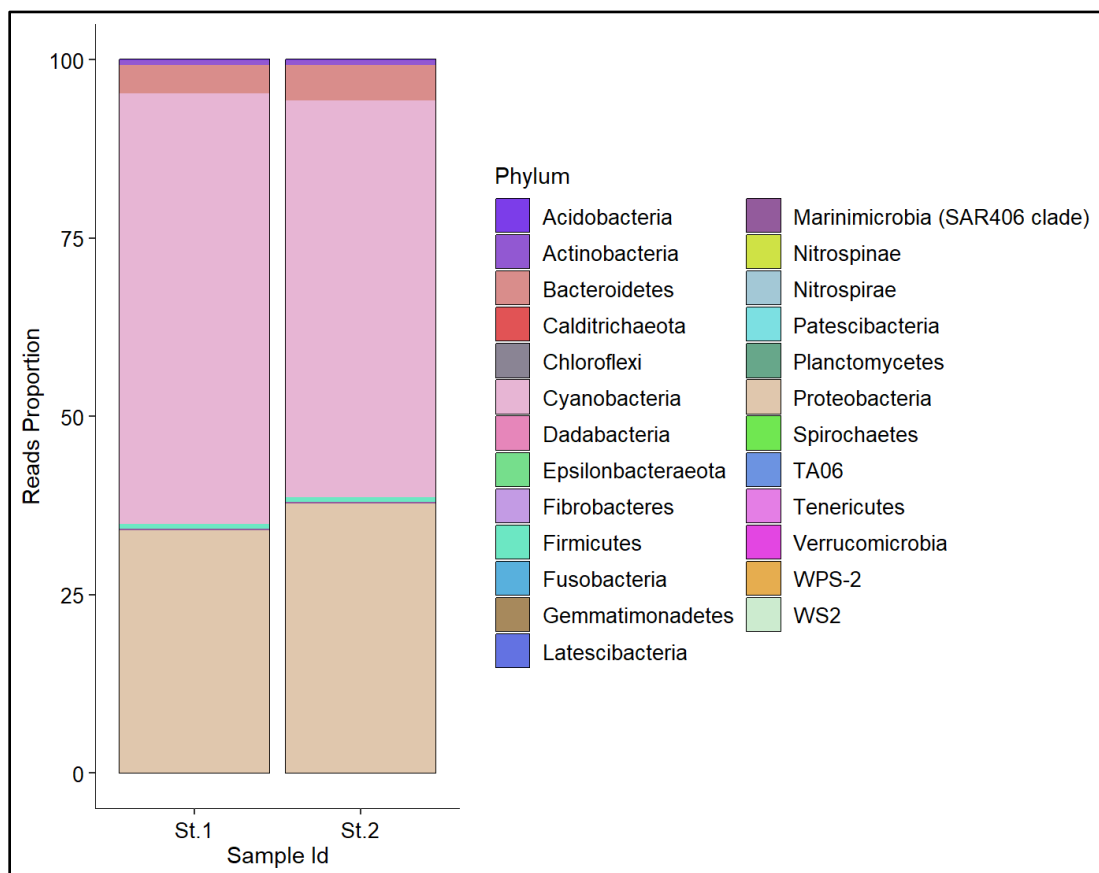


Figure 2. Taxa identified at the phylum level across all samples based on read proportion.

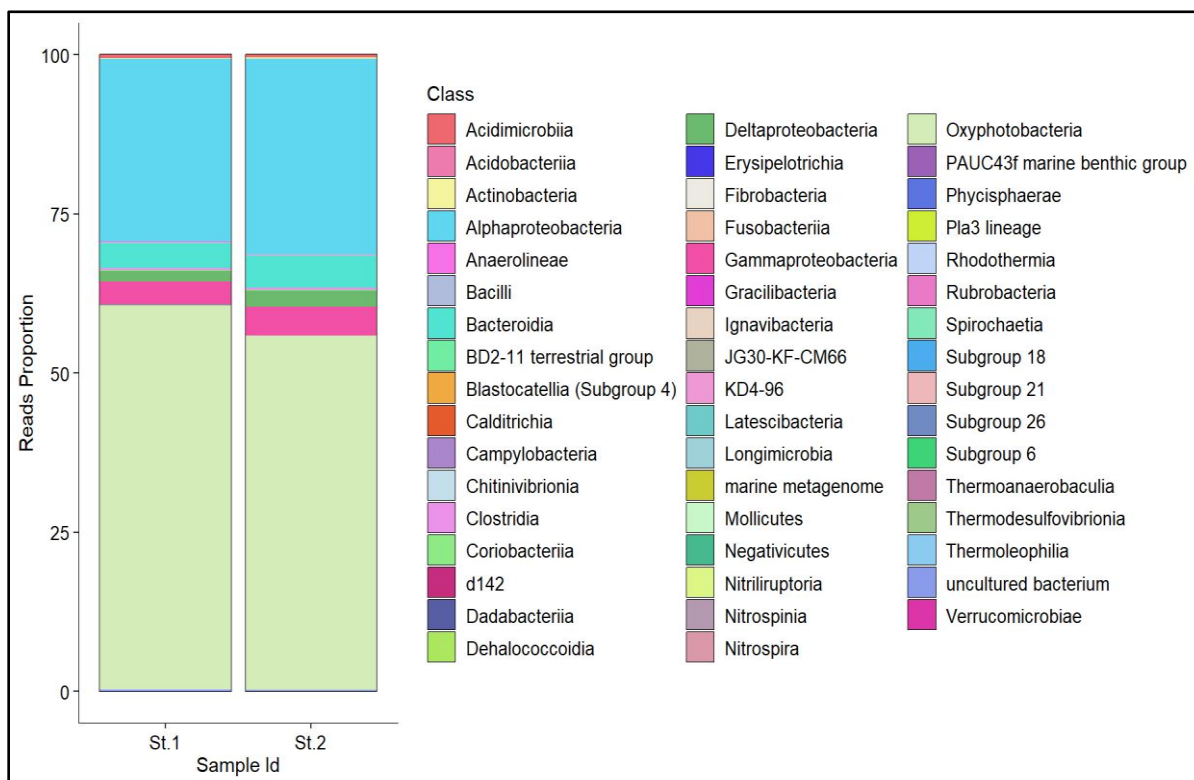


Figure 3. Taxa identified at the class level across all samples based on read proportion.

The Krona chart (Figure 4) at site 1, located near the seabed in the cultivation region of *K. alvarezii* infected with ice-ice, shows that 60% of the total bacteria detected were Oxyphotobacteria (phylum Cyanobacteria). Among these, 54% were *Synechococcus* CC9902, 2% were *Cyanobium* PCC-6307, and 4% were other types. Subsequently, the phylum Proteobacteria comprises 34% of the total, with 28% being Alphaproteobacteria, 4% Gammaproteobacteria, and 2% Deltaproteobacteria. Within the class Gammaproteobacteria, 0.1% were comprised by *Vibrio* (339 bacteria), which included *Vibrio azureus*, *Vibrio* sp. S573, and *Vibrio aerogenes*. Furthermore, the phylum Bacteroidetes accounts for up to 4%.

At site 2, located at a depth of around 30-50 cm (which corresponds to the depth of *K. alvarezii* cultivation), the investigation revealed 56% Cyanobacteria, 38% Proteobacteria, and 5% Bacteroidetes. The discovered phylum Cyanobacteria consists of the class Oxyphotobacteria, which includes the genus *Synechococcus* CC9902 (43%) and other genera. Within the phylum Proteobacteria, Alphaproteobacteria accounts for 31%, Gammaproteobacteria for 5%, and Deltaproteobacteria for 3% of the phylum. Within the Gammaproteobacteria class, a total of 0.3% were identified as *Vibrio* (495 bacteria), including *Vibrio azureus*, *Vibrio* sp. S573, *Vibrio aerogenes*, and uncultured *Vibrio* sp. Apart from *Vibrio* at site 2, uncultured *Pseudoalteromonas* sp. was also present in tiny amounts.



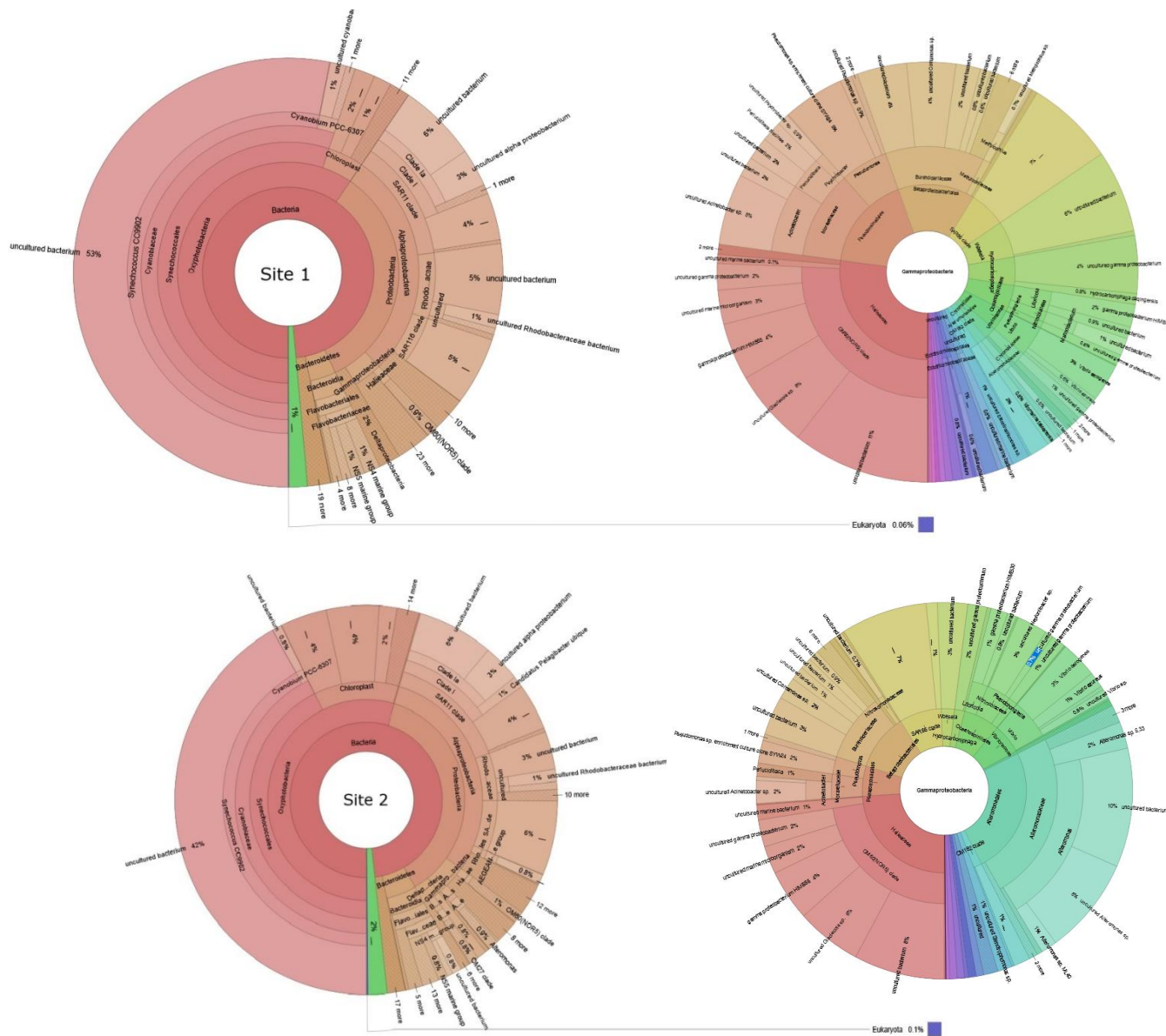


Figure 4. Krona plots visualizing taxonomic hierarchies based on read proportions for each sample.

Table 1

List of all identified taxa from sample against database with 97% similarity sequence

<i>Phylum</i>	<i>Class</i>	<i>Order</i>	<i>Family</i>	<i>Genus</i>	<i>Species</i>
Acidobacteria	Blastocatellia (Subgroup 4)	Blastocatellales	Blastocatellaceae	<i>Blastocatella</i>	<i>Blastocatella</i> sp.
Acidobacteria	Acidobacteriia	Solibacterales	Solibacteraceae (Subgroup 3)	<i>Bryobacter</i>	<i>Bryobacter</i> sp.
Acidobacteria	Subgroup 26	uncultured Acidobacteria bacterium	NA	NA	NA
Acidobacteria	Subgroup 26	uncultured Acidobacteriaceae bacterium	NA	NA	NA
Acidobacteria	d142	uncultured organism	NA	NA	NA
Acidobacteria	Subgroup 21	uncultured bacterium	NA	NA	NA
Acidobacteria	Subgroup 18	uncultured bacterium	NA	NA	NA
Acidobacteria	Subgroup 6	uncultured bacterium	NA	NA	NA
Acidobacteria	Thermoanaerobaculia	Thermoanaerobaculales	Thermoanaerobaculaceae	Subgroup 10	uncultured <i>Acidobacteria</i> bacterium
Acidobacteria	Thermoanaerobaculia	Thermoanaerobaculales	Thermoanaerobaculaceae	Subgroup 10	uncultured bacterium
Actinobacteria	Acidimicrobiia	Actinomarinales	Actinomarinaceae	<i>Candidatus Actinomarina</i>	<i>Candidatus Actinomarina</i> sp.
Actinobacteria	Coriobacteriia	Coriobacteriales	Coriobacteriaceae	<i>Collinsella</i>	<i>Collinsella</i> sp.
Actinobacteria	Actinobacteria	Propionibacteriales	Propionibacteriaceae	<i>Cutibacterium</i>	<i>Cutibacterium</i> sp.
Actinobacteria	Actinobacteria	Corynebacteriales	Nocardiaceae	<i>Gordonia</i>	<i>Gordonia</i> sp.
Actinobacteria	Actinobacteria	Micrococcales	Promicromonosporaceae	<i>Isoptericola</i>	<i>Isoptericola</i> sp.
Actinobacteria	Actinobacteria	Micrococcales	Microbacteriaceae	<i>Microbacterium</i>	<i>Microbacterium</i> sp.
Actinobacteria	Actinobacteria	PeM15	metagenome	NA	NA
Actinobacteria	Actinobacteria	PeM15	uncultured bacterium	NA	NA
Actinobacteria	Actinobacteria	PeM15	uncultured bacterium	NA	NA
Actinobacteria	Actinobacteria	PeM15	ARCTIC38_F_05	NA	NA
Actinobacteria	Actinobacteria	Actinomarinales	uncultured bacterium	NA	NA
Actinobacteria	Actinobacteria	Propionibacteriales	Nocardioidaceae	<i>Nocardioides</i>	<i>Nocardioides</i> sp.
Actinobacteria	Rubrobacteria	Rubrobacteriales	Rubrobacteriaceae	<i>Rubrobacter</i>	<i>Rubrobacter aplysinae</i>
Actinobacteria	Actinobacteria	Micrococcales	Sanguibacteraceae	<i>Sanguibacter</i>	<i>Sanguibacter</i> sp.
Actinobacteria	Actinobacteria	Micrococcales	Intrasporangiaceae	<i>Serinicoccus</i>	<i>Serinicoccus</i> sp.
Actinobacteria	Nitriliruptoria	Nitriliruptorales	Nitriliruptoraceae	soda lake metagenome	NA
Actinobacteria	Acidimicrobiia	Microtrichales	Microtrichaceae	Sva0996 marine group	uncultured actinobacterium
Actinobacteria	Acidimicrobiia	Microtrichales	Microtrichaceae	Sva0996 marine group	uncultured bacterium
Actinobacteria	Acidimicrobiia	Microtrichales	Ilumatobacteraceae	uncultured	uncultured actinobacterium
Actinobacteria	Acidimicrobiia	Microtrichales	Ilumatobacteraceae	uncultured	uncultured bacterium

<i>Phylum</i>	<i>Class</i>	<i>Order</i>	<i>Family</i>	<i>Genus</i>	<i>Species</i>
Actinobacteria	Acidimicrobiia	Actinomarinales	uncultured	uncultured actinobacterium	NA
Actinobacteria	Thermoleophilia	Solirubrobacterales	67-14	uncultured actinobacterium	NA
Actinobacteria	Acidimicrobiia	Actinomarinales	uncultured	uncultured bacterium	NA
Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	<i>Actibacter</i>	uncultured Bacteroidetes bacterium
Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	<i>Aquibacter</i>	<i>Aquibacter</i> sp.
Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	<i>Aureicoccus</i>	<i>Aureicoccus</i> sp.
Bacteroidetes	Bacteroidia	Chitinophagales	Saprospiraceae	<i>Aureispira</i>	<i>Aureispira</i> sp.
Bacteroidetes	Rhodothermia	Balneolales	Balneolaceae	B2706-C7	uncultured bacterium
Bacteroidetes	Rhodothermia	Balneolales	Balneolaceae	<i>Balneola</i>	<i>Balneola</i> sp.
Bacteroidetes	Bacteroidia	Flavobacteriales	Weeksellaceae	<i>Cloacibacterium</i>	<i>Cloacibacterium</i> sp.
Bacteroidetes	Bacteroidia	Flavobacteriales	Crocinitomicaceae	<i>Crocinitomix</i>	<i>Crocinitomix</i> sp.
Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	<i>Dokdonia</i>	<i>Dokdonia</i> sp.
Bacteroidetes	Bacteroidia	Cytophagales	Cyclobacteriaceae	<i>Ekhidna</i>	<i>Ekhidna</i> sp.
Bacteroidetes	Bacteroidia	Cytophagales	Spirosomaceae	<i>Emticicia</i>	<i>Emticicia</i> sp.
Bacteroidetes	Bacteroidia	Cytophagales	Cyclobacteriaceae	<i>Fabibacter</i>	<i>Flammeovirgaceae</i> bacterium
Bacteroidetes	Bacteroidia	Flavobacteriales	Crocinitomicaceae	<i>Fluviicola</i>	<i>Fluviicola</i> sp.
Bacteroidetes	Bacteroidia	Cytophagales	Cyclobacteriaceae	<i>Fulvivirga</i>	<i>Fulvivirga</i> sp.
Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	<i>Gilvibacter</i>	uncultured bacterium
Bacteroidetes	Bacteroidia	Chitinophagales	Saprospiraceae	<i>Lewinella</i>	<i>Lewinella</i> sp.
Bacteroidetes	Bacteroidia	Chitinophagales	uncultured	metagenome	NA
Bacteroidetes	Bacteroidia	Cytophagales	Cyclobacteriaceae	<i>Marinoscillum</i>	<i>Marinoscillum</i> sp.
Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	<i>Muricauda</i>	<i>Bacteroidetes</i> bacterium JS5
Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	<i>Muricauda</i>	<i>Flavobacteriaceae</i> bacterium GUDS972
Bacteroidetes	Bacteroidia	Chitinophagales	Chitinophagaceae	<i>Niabella</i>	<i>Niabella yanshanensis</i>
Bacteroidetes	Bacteroidia	Flavobacteriales	Cryomorphaceae	NS10 marine group	uncultured bacterium
Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	NS2b marine group	uncultured bacterium
Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	NS2b marine group	uncultured marine bacterium
Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	NS4 marine group	uncultured bacterium
Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	NS4 marine group	uncultured marine bacterium
Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	NS5 marine group	uncultured bacterium
Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	NS5 marine group	uncultured Bacteroidetes/Chlorobi group bacterium
Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	NS5 marine group	uncultured bacterium
Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	NS5 marine group	<i>Flavobacteriaceae</i> bacterium



<i>Phylum</i>	<i>Class</i>	<i>Order</i>	<i>Family</i>	<i>Genus</i>	<i>Species</i>
Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	NS5 marine group	uncultured marine bacterium
Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	NS5 marine group	uncultured marine microorganism
Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	<i>Prevotella</i>	<i>Prevotella</i> sp.
Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	Prevotellaceae NK3B31 group	uncultured bacterium
Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	Prevotellaceae UCG-003	uncultured bacterium
Bacteroidetes	Bacteroidia	Cytophagales	Cyclobacteriaceae	<i>Reichenbachiella</i>	<i>Reichenbachiella</i> sp.
Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Rikenellaceae RC9 gut group	uncultured bacterium
Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	<i>Robiginitalea</i>	<i>Robiginitalea</i> sp.
Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	<i>Robiginitalea</i>	<i>Robiginitalea myxolifaciens</i>
Bacteroidetes	Rhodothermia	Rhodothermales	Rhodothermaceae	<i>Rubrivirga</i>	<i>Rubrivirga marina</i>
Bacteroidetes	Bacteroidia	Cytophagales	Spirosomaceae	<i>Runella</i>	<i>Runella</i> sp.
Bacteroidetes	Bacteroidia	Chitinophagales	Saprospiraceae	<i>Saprospira</i>	<i>Saprospira</i> sp.
Bacteroidetes	Bacteroidia	Chitinophagales	Chitinophagaceae	<i>Sediminibacterium</i>	<i>Sediminibacterium</i> sp.
Bacteroidetes	Bacteroidia	Chitinophagales	Chitinophagaceae	<i>Taibaiella</i>	<i>Taibaiella</i> sp.
Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	<i>Tenacibaculum</i>	<i>Tenacibaculum</i> sp.
Bacteroidetes	Bacteroidia	Chitinophagales	Chitinophagaceae	uncultured	metagenome
Bacteroidetes	Bacteroidia	Chitinophagales	Saprospiraceae	<i>Tetraselmis</i>	<i>Tetraselmis</i> sp.
Bacteroidetes	Bacteroidia	Cytophagales	Cyclobacteriaceae	uncultured	uncultured bacterium
Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	uncultured	uncultured bacterium
Bacteroidetes	Bacteroidia	Chitinophagales	Saprospiraceae	uncultured	uncultured bacterium
Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	uncultured	uncultured bacterium
Bacteroidetes	Bacteroidia	Flavobacteriales	Cryomorphaceae	uncultured	uncultured bacterium
Bacteroidetes	Bacteroidia	Flavobacteriales	Cryomorphaceae	uncultured	<i>Bacteroidetes bacterium</i>
Bacteroidetes	Bacteroidia	Cytophagales	Cyclobacteriaceae	uncultured	uncultured
Bacteroidetes	Bacteroidia	Cytophagales	Cyclobacteriaceae	uncultured	Flammeovirgaceae bacterium
Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	uncultured	uncultured
Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	uncultured	Flavobacteriaceae bacterium
Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	uncultured	uncultured
Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	uncultured	Flavobacteriales bacterium
Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	<i>Flavobacterium</i>	<i>Flavobacterium</i> sp.
Bacteroidetes	Bacteroidia	Chitinophagales	Saprospiraceae	uncultured	uncultured marine bacterium
Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	uncultured	uncultured marine microorganism
Bacteroidetes	Bacteroidia	Bacteroidales	Prolixibacteraceae	uncultured	uncultured organism
Bacteroidetes	Bacteroidia	Flavobacteriales	Cryomorphaceae	uncultured	uncultured organism

<i>Phylum</i>	<i>Class</i>	<i>Order</i>	<i>Family</i>	<i>Genus</i>	<i>Species</i>
Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	uncultured bacterium	NA
Bacteroidetes	Bacteroidia	Flavobacteriales	NS9 marine group	uncultured bacterium	NA
Bacteroidetes	Ignavibacteria	Kryptoniales	BSV26	uncultured bacterium	NA
Bacteroidetes	Bacteroidia	Flavobacteriales	NS7 marine group	uncultured bacterium	NA
Bacteroidetes	Bacteroidia	Sphingobacteriales	Lentimicrobiaceae	uncultured bacterium	NA
Bacteroidetes	Bacteroidia	Flavobacteriales	NS9 marine group	uncultured deep-sea bacterium	NA
Bacteroidetes	Bacteroidia	Flavobacteriales	NS9 marine group	uncultured marine bacterium	NA
Bacteroidetes	Bacteroidia	Bacteroidales	Muribaculaceae	uncultured organism	NA
Bacteroidetes	Bacteroidia	Chitinophagales	uncultured	uncultured Sphingobacteriales bacterium	NA
Bacteroidetes	Bacteroidia	Sphingobacteriales	NS11-12 marine group	uncultured Sphingobacterium	NA
Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	<i>Wenyngzhuangia</i>	<i>Ochrovirga pacifica</i>
Bacteroidetes	Bacteroidia	Flavobacteriales	Flavobacteriaceae	<i>Zeaxanthinibacter</i>	<i>Zeaxanthinibacter</i> sp.
Calditrichaeota	Calditrichia	Calditrichales	Calditrichaceae	uncultured bacterium	NA
Chloroflexi	Dehalococcoidia	SAR202 clade	uncultured bacterium	NA	NA
Chloroflexi	Dehalococcoidia	S085	uncultured bacterium	NA	NA
Chloroflexi	Anaerolineae	uncultured	uncultured bacterium	NA	NA
Chloroflexi	KD4-96	uncultured bacterium	NA	NA	NA
Chloroflexi	JG30-KF-CM66	uncultured bacterium	NA	NA	NA
Chloroflexi	Anaerolineae	SBR1031	uncultured bacterium	NA	NA
Chloroflexi	Anaerolineae	Anaerolineales	Anaerolineaceae	uncultured bacterium	uncultured bacterium
Chloroflexi	Anaerolineae	Ardenticatenales	uncultured	uncultured bacterium	NA
Cyanobacteria	Oxyphotobacteria	Phormidesmiales	Phormidesmiaceae	<i>Acrophormium</i>	<i>Acrophormium</i> sp.
Cyanobacteria	Oxyphotobacteria	Nostocales	Coleofasciculaceae	<i>Coleofasciculus</i>	uncultured cyanobacterium
Cyanobacteria	Oxyphotobacteria	Synechococcales	Cyanobiaceae	PCC-7420 <i>Cyanobium</i>	<i>Cyanobium</i> sp.
Cyanobacteria	Oxyphotobacteria	Synechococcales	Cyanobiaceae	<i>Cyanobium</i> PCC-6307	uncultured cyanobacterium
Cyanobacteria	Oxyphotobacteria	Chloroplast	uncultured phototrophic eukaryote	NA	NA
Cyanobacteria	Oxyphotobacteria	Chloroplast	uncultured marine eukaryote	NA	NA
Cyanobacteria	Oxyphotobacteria	Chloroplast	uncultured bacterium	NA	NA
Cyanobacteria	Oxyphotobacteria	Chloroplast	unidentified eukaryote clone OM21	NA	NA

<i>Phylum</i>	<i>Class</i>	<i>Order</i>	<i>Family</i>	<i>Genus</i>	<i>Species</i>
Cyanobacteria	Oxyphotobacteria	Chloroplast	Thalassiosira weissflogii	NA	NA
Cyanobacteria	Oxyphotobacteria	Chloroplast	uncultured marine microorganism	NA	NA
Cyanobacteria	Oxyphotobacteria	Chloroplast	Picochlorum sp. SENEW3	NA	NA
Cyanobacteria	Oxyphotobacteria	Chloroplast	Marsupiomonas sp. NIES 1824	NA	NA
Cyanobacteria	Oxyphotobacteria	Chloroplast	Chlorarachnion sp. CCMP242	NA	NA
Cyanobacteria	Oxyphotobacteria	Chloroplast	Proteomonas sulcata	NA	NA
Cyanobacteria	Oxyphotobacteria	Chloroplast	marine metagenome	NA	NA
Cyanobacteria	Oxyphotobacteria	Chloroplast	uncultured organism	NA	NA
Cyanobacteria	Oxyphotobacteria	Chloroplast	uncultured diatom	NA	NA
Cyanobacteria	Oxyphotobacteria	Chloroplast	uncultured cyanobacterium	NA	NA
Cyanobacteria	Oxyphotobacteria	Chloroplast	Chlorella variabilis	NA	NA
Cyanobacteria	Oxyphotobacteria	Chloroplast	metagenome	NA	NA
Cyanobacteria	Oxyphotobacteria	Chloroplast	unidentified marine bacterioplankton	NA	NA
Cyanobacteria	Oxyphotobacteria	Chloroplast	Tetraselmis sp. GSL018	NA	NA
Cyanobacteria	Oxyphotobacteria	Chloroplast	Guillardia theta	NA	NA
Cyanobacteria	Oxyphotobacteria	Nostocales	Oscillatoriaceae	<i>Phormidium</i> ETS-05	<i>Phormidium</i> sp.
Cyanobacteria	Oxyphotobacteria	Synechococcales	Synechococcales Incertae Sedis	<i>Schizothrix</i>	<i>Schizothrix</i> sp.
Cyanobacteria	Oxyphotobacteria	Nostocales	Paraspirulinaceae	<i>Spirulina</i>	<i>Spirulina</i> sp.
Cyanobacteria	Oxyphotobacteria	Nostocales	Cyanobacteriaceae	<i>Symphothece</i> PCC-7002	<i>Limnothrix rosea</i> IAM M-220
Cyanobacteria	Oxyphotobacteria	Synechococcales	Cyanobiaceae	<i>Synechococcus</i>	<i>Synechococcus</i> sp.
Cyanobacteria	Oxyphotobacteria	Eurycoccales	Eurycoccales Incertae Sedis	<i>Synechococcus</i>	<i>Synechococcus</i> sp.
Cyanobacteria	Oxyphotobacteria	Nostocales	Phormidiaceae	<i>Trichodesmium</i> IMS101	<i>Oscillatoria miniata</i> NAC8-50
Dadabacteria	Dadabacteriia	Dadabacteriales	uncultured bacterium	NA	NA
Epsilonbacteraeota	Campylobacteria	Campylobacteriales	Arcobacteraceae	<i>Arcobacter</i>	<i>Arcobacter</i> sp.
Epsilonbacteraeota	Campylobacteria	Campylobacteriales	Thiovulaceae	<i>Sulfurimonas</i>	uncultured bacterium
Epsilonbacteraeota	Campylobacteria	Campylobacteriales	Thiovulaceae	<i>Sulfurimonas</i>	uncultured <i>Sulfurimonas</i> sp.
Fibrobacteres	Chitinivibrionia	Chitinivibrionales	Chitinivibrionaceae	possible genus 03	uncultured bacterium
Fibrobacteres	Fibrobacteria	Fibrobacterales	Fibrobacteraceae	uncultured	uncultured bacterium
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	[ <i>Ruminococcus</i> ] gauvreauii group	uncultured bacterium
Firmicutes	Negativicutes	Selenomonadales	Veillonellaceae	<i>Anaerovibrio</i>	<i>Anaerovibrio</i> sp.
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	<i>Blautia</i>	<i>Blautia</i> sp.
Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	<i>Catenibacterium</i>	<i>Catenibacterium</i> sp.
Firmicutes	Bacilli	Bacillales	Family XII	<i>Exiguobacterium</i>	<i>Exiguobacterium</i> sp.
Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	<i>Lactobacillus</i>	<i>Lactobacillus</i> sp.
Firmicutes	Bacilli	Bacillales	Bacillaceae	<i>Marinococcus</i>	<i>Marinococcus luteus</i>

<i>Phylum</i>	<i>Class</i>	<i>Order</i>	<i>Family</i>	<i>Genus</i>	<i>Species</i>
Firmicutes	Bacilli	Bacillales	Paenibacillaceae	<i>Paenibacillus</i>	<i>Paenibacillus</i> sp.
Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	<i>Romboutsia</i>	<i>Romboutsia</i> sp.
Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	<i>Ruminococcaceae</i> UCG-005	uncultured bacterium
Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	<i>Ruminococcaceae</i> UCG-008	uncultured bacterium
Firmicutes	Bacilli	Bacillales	Staphylococcaceae	<i>Staphylococcus</i>	<i>Staphylococcus</i> sp.
Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	<i>Streptococcus</i>	uncultured bacterium
Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	<i>Subdoligranulum</i>	uncultured bacterium
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	uncultured	uncultured bacterium
Firmicutes	Clostridia	Clostridiales	Eubacteriaceae	uncultured bacterium	NA
Fusobacteria	Fusobacteriia	Fusobacteriales	Fusobacteriaceae	<i>Propionigenium</i>	<i>Propionigenium</i> sp.
Fusobacteria	Fusobacteriia	Fusobacteriales	Leptotrichiaceae	<i>Leptotrichia</i>	<i>Leptotrichia</i> sp.
Gemmatimonadetes	BD2-11 terrestrial group	uncultured bacterium	NA	NA	NA
Gemmatimonadetes	PAUC43f marine benthic group	uncultured bacterium	NA	NA	NA
Gemmatimonadetes	Longimicrobia	Longimicrobiales	Longimicrobiaceae	uncultured bacterium	NA
Latescibacteria	uncultured bacterium	NA	NA	NA	NA
Latescibacteria	Latescibacteria	Latescibacterales	Latescibacteraceae	uncultured bacterium	NA
Marinimicrobia (SAR406 clade)	uncultured bacterium	NA	NA	NA	NA
Nitrospinae	Nitrospina	Nitrospinales	Nitrospinae	<i>Nitrospina</i>	<i>Nitrospina</i> sp.
Nitrospirae	Thermodesulfovibronia	uncultured	uncultured bacterium	NA	NA
Nitrospirae	Nitrospira	Nitrospirales	Nitrospiraceae	<i>Nitrospira</i>	<i>Nitrospira</i> sp.
Patescibacteria	Gracilibacteria	Absconditabacteriales (SR1)	uncultured organism	NA	NA
Patescibacteria	Gracilibacteria	Candidatus Peregrinibacteria	uncultured bacterium	NA	NA
Patescibacteria	Gracilibacteria	JGI 0000069-P22	uncultured bacterium	NA	NA
Patescibacteria	Gracilibacteria	uncultured bacterium	NA	NA	NA
Patescibacteria	Gracilibacteria	Candidatus Peribacteria	uncultured bacterium	NA	NA
Planctomycetes	Pla3 lineage	uncultured bacterium	NA	NA	NA
Planctomycetes	Phycisphaerae	Phycisphaerales	Phycisphaeraceae	uncultured	uncultured bacterium
Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	<i>Achromobacter</i>	uncultured <i>Achromobacter</i> sp.
Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	<i>Achromobacter</i>	<i>Achromobacter</i> sp.
Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	<i>Acidovorax</i>	<i>Acidovorax</i> sp. uncultured
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	<i>Acinetobacter</i>	<i>Acinetobacter</i> sp.
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	<i>Acinetobacter</i>	<i>Acinetobacter</i> sp.
Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Actibacterium</i>	uncultured alpha proteobacterium
Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Actibacterium</i>	<i>Actibacterium</i> sp.

<i>Phylum</i>	<i>Class</i>	<i>Order</i>	<i>Family</i>	<i>Genus</i>	<i>Species</i>
Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	<i>Aestuariibacter</i>	<i>Aestuariibacter</i> sp.
Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	<i>Agaribacter</i>	<i>Alteromonas</i> sp.
Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	<i>Aliiglaciicola</i>	<i>Aliiglaciicola</i> sp.
Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	<i>Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium</i>	<i>Allorhizobium-Neorhizobium</i>
Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	<i>Alteromonas</i>	<i>Alteromonas</i> sp. uncultured
Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	<i>Alteromonas</i>	<i>Alteromonas</i> sp.
Proteobacteria	Gammaproteobacteria	Aeromonadales	Succinivibrionaceae	<i>Anaerobiospirillum</i>	<i>Anaerobiospirillum succiniciproducens</i>
Proteobacteria	Gammaproteobacteria	Nitrosococcales	Nitrosococcaceae	AqS1	uncultured bacterium
Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	<i>Aquabacterium</i>	<i>Aquabacterium</i> sp.
Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Asciadiaceihabitans</i>	<i>Asciadiaceihabitans</i> sp.
Proteobacteria	Alphaproteobacteria	Azospirillales	Azospirillaceae	<i>Azospirillum</i>	<i>Azospirillum</i> sp.
Proteobacteria	Deltaproteobacteria	Bdellovibrionales	Bdellovibrionaceae	<i>Bdellovibrio</i>	<i>Bdellovibrio</i> sp.
Proteobacteria	Alphaproteobacteria	Rhizobiales	Xanthobacteraceae	<i>Bradyrhizobium</i>	<i>Bradyrhizobium</i> sp.
Proteobacteria	Alphaproteobacteria	Rhizobiales	Stappiaceae	<i>Breoghania</i>	<i>Breoghania</i> sp.
Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	<i>Brevundimonas</i>	<i>Brevundimonas</i> sp.
Proteobacteria	Gammaproteobacteria	Chromatiales	Chromatiaceae	<i>Candidatus Thiobios</i>	<i>Candidatus thiobios</i> sp.
Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	<i>Caulobacter</i>	<i>Caulobacter</i> sp. uncultured alpha proteobacterium
Proteobacteria	Alphaproteobacteria	SAR11 clade	Clade I	Clade Ia	uncultured alpha proteobacterium
Proteobacteria	Alphaproteobacteria	SAR11 clade	Clade I	Clade Ia	uncultured bacterium
Proteobacteria	Alphaproteobacteria	SAR11 clade	Clade I	<i>Candidatus Pelagibacter</i>	<i>Candidatus Pelagibacter ubique</i>
Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	<i>Cohaesibacter</i>	<i>Cohaesibacter</i> sp.
Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	<i>Comamonas</i>	<i>Comamonas</i> sp.
Proteobacteria	Gammaproteobacteria	Coxiellales	Coxiellaceae	<i>Coxiella</i>	<i>Coxiella</i> sp.
Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	<i>Cupriavidus</i>	<i>Cupriavidus gilardii</i>
Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	<i>Curvibacter</i>	<i>Curvibacter</i> sp.
Proteobacteria	Deltaproteobacteria	Deltaproteobacteria Incertae Sedis	Unknown Family	<i>Deferrisoma</i>	<i>Deferrisoma</i> sp.
Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	<i>Delftia</i>	<i>Delftia</i> sp.
Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Donghicola</i>	<i>Donghicola</i> sp.
Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Epibacterium</i>	<i>Epibacterium ulvae</i>
Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	<i>Erythrobacter</i>	<i>Erythrobacter</i> sp.
Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	<i>Filomicrobium</i>	<i>Filomicrobium</i> sp.
Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	<i>Filomicrobium</i>	<i>Hyphomicrobiaceae bacterium</i>
Proteobacteria	Gammaproteobacteria	Cellvibrionales	Haliaceae	<i>Halioglobus</i>	<i>Halioglobus</i> sp.
Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	<i>Halomonas</i>	<i>Halomonas</i> sp.
Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	HIMB11	uncultured bacterium
Proteobacteria	Gammaproteobacteria	Salinisphaerales	Solimonadaceae	<i>Hydrocarboniphaga</i>	<i>Hydrocarboniphaga daqingensis</i>

<i>Phylum</i>	<i>Class</i>	<i>Order</i>	<i>Family</i>	<i>Genus</i>	<i>Species</i>
Proteobacteria	Gammaproteobacteria	Salinisphaerales	Solimonadaceae	<i>Hydrocarboniphaga</i>	<i>Hydrocarboniphaga</i> sp.
Proteobacteria	Alphaproteobacteria	Caulobacterales	Hyphomonadaceae	<i>Hyphobacterium</i>	<i>Hyphobacterium</i> sp.
Proteobacteria	Alphaproteobacteria	Caulobacterales	Hyphomonadaceae	<i>Hyphomonas</i>	<i>Hyphomonas</i> sp.
Proteobacteria	Gammaproteobacteria	Alteromonadales	Idiomarinaeae	<i>Idiomarina</i>	<i>Idiomarina taiwanensis</i>
Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Nitrosomonadaceae	IS-44	uncultured bacterium
Proteobacteria	Alphaproteobacteria	Kordiimonadales	Kordiimonadaceae	<i>Kordiimonas</i>	<i>Kordiimonas</i> sp.
Proteobacteria	Alphaproteobacteria	Rhizobiales	Stappiaceae	<i>Labrenzia</i>	<i>Labrenzia</i> sp.
Proteobacteria	Gammaproteobacteria	Legionellales	Legionellaceae	<i>Legionella</i>	<i>Legionella</i> sp.
Proteobacteria	Alphaproteobacteria	Rhodovibrionales	Kiloniellaceae	<i>Limibacillus</i>	<i>Limibacillus</i> sp.
Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	<i>Limnobacter</i>	<i>Limnobacter</i> sp.
Proteobacteria	Gammaproteobacteria	Oceanospirillales	Litoricolaceae	<i>Litoricola</i>	<i>Litoricola</i> sp.
Proteobacteria	Gammaproteobacteria	Cellvibrionales	Haliaceae	<i>Luminiphilus</i>	uncultured marine bacterium
Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Mameliella</i>	<i>Mameliella</i> sp.
Proteobacteria	Alphaproteobacteria	Caulobacterales	Hyphomonadaceae	<i>Maricaulis</i>	<i>Maricaulis</i> sp.
Proteobacteria	Gammaproteobacteria	Oceanospirillales	Nitrincolaceae	<i>Marinobacterium</i>	<i>Marinobacterium</i> sp.
Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	<i>Marispirillum</i>	<i>Marispirillum indicum</i>
Proteobacteria	Alphaproteobacteria	Rickettsiales	Midichloriaceae	MD3-55	uncultured bacterium
Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	<i>Mesorhizobium</i>	<i>Mesorhizobium</i> sp.
Proteobacteria	Alphaproteobacteria	Rickettsiales	Mitochondria	<i>metagenome</i>	NA
Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiacae	<i>Methylobacterium</i>	<i>Methylobacterium</i> sp.
Proteobacteria	Gammaproteobacteria	Nitrosococcales	Methylophagaceae	<i>Methylophaga</i>	<i>Methylophaga</i> sp.
Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Methylophilaceae	<i>Methylophilus</i>	<i>Methylophilus flavus</i>
Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Methylophilaceae	<i>Methylophilus</i>	<i>Methylophilus</i> sp.
Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Rhodocyclaceae	<i>Methyloversatilis</i>	<i>Methyloversatilis</i> sp.
Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Nitrosomonadaceae	mle1-7	uncultured bacterium
Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	MWH-UniP1 aquatic group	uncultured bacterium
Proteobacteria	Deltaproteobacteria	PB19	uncultured bacterium	NA	NA
Proteobacteria	Deltaproteobacteria	NB1-j	uncultured bacterium	NA	NA
Proteobacteria	Gammaproteobacteria	B2M28	uncultured bacterium	NA	NA
Proteobacteria	Alphaproteobacteria	uncultured	uncultured	NA	NA
Proteobacteria	Alphaproteobacteria	uncultured	Rhodospirillales bacterium	NA	NA
Proteobacteria	Deltaproteobacteria	Bradymonadales	uncultured bacterium	NA	NA
Proteobacteria	Deltaproteobacteria	Sva0485	uncultured bacterium	NA	NA
Proteobacteria	Deltaproteobacteria	PB19	uncultured delta proteobacterium	NA	NA
Proteobacteria	Gammaproteobacteria	BD7-8	uncultured bacterium	NA	NA
Proteobacteria	Alphaproteobacteria	uncultured	uncultured bacterium	NA	NA
Proteobacteria	Deltaproteobacteria	SAR324 clade(Marine group B)	uncultured bacterium	NA	NA
Proteobacteria	Gammaproteobacteria	pItb-vmat-80	uncultured gamma proteobacterium	NA	NA
Proteobacteria	Gammaproteobacteria	SAR86 clade	uncultured bacterium	NA	NA
Proteobacteria	Gammaproteobacteria	uncultured	uncultured bacterium	NA	NA



<i>Phylum</i>	<i>Class</i>	<i>Order</i>	<i>Family</i>	<i>Genus</i>	<i>Species</i>
Proteobacteria	Deltaproteobacteria	MBNT15	uncultured bacterium	NA	NA
Proteobacteria	Alphaproteobacteria	uncultured	uncultured Phyllobacteriaceae bacterium	NA	NA
Proteobacteria	Gammaproteobacteria	OM182 clade	unidentified marine bacterioplankton	NA	NA
Proteobacteria	Alphaproteobacteria	uncultured	uncultured deep-sea bacterium	NA	NA
Proteobacteria	Deltaproteobacteria	Bradymonadales	uncultured marine bacterium	NA	NA
Proteobacteria	Alphaproteobacteria	uncultured	uncultured alpha proteobacterium	NA	NA
Proteobacteria	Gammaproteobacteria	SAR86 clade	uncultured gamma proteobacterium	NA	NA
Proteobacteria	Deltaproteobacteria	PB19	uncultured marine microorganism	NA	NA
Proteobacteria	Gammaproteobacteria	HOC36	uncultured bacterium	NA	NA
Proteobacteria	Gammaproteobacteria	OM182 clade	uncultured marine bacterium	NA	NA
Proteobacteria	Gammaproteobacteria	Ga0077536	uncultured bacterium	NA	NA
Proteobacteria	Gammaproteobacteria	Gammaproteobacteria Incertae Sedis	NA	NA	NA
Proteobacteria	Gammaproteobacteria	Oceanospirillales	Nitrincolaceae	<i>Neptuniibacter</i>	<i>Neptuniibacter</i> sp.
Proteobacteria	Alphaproteobacteria	Azospirillales	Azospirillaceae	<i>Niveispirillum</i>	<i>Azospirillum</i> sp.
Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	<i>Novosphingobium</i>	<i>Novosphingobium</i> sp.
Proteobacteria	Deltaproteobacteria	Bdellovibrionales	Bdellovibrionaceae	OM27 clade	uncultured bacterium
Proteobacteria	Deltaproteobacteria	Bdellovibrionales	Bdellovibrionaceae	OM27 clade	uncultured delta proteobacterium
Proteobacteria	Deltaproteobacteria	Bdellovibrionales	Bdellovibrionaceae	OM27 clade	uncultured marine bacterium
Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Methylophilaceae	OM43 clade	uncultured bacterium gamma proteobacterium
Proteobacteria	Gammaproteobacteria	Cellvibrionales	Haliaceae	OM60(NOR5) clade	HIMB55
Proteobacteria	Gammaproteobacteria	Cellvibrionales	Haliaceae	OM60(NOR5) clade	uncultured bacterium
Proteobacteria	Gammaproteobacteria	Cellvibrionales	Haliaceae	OM60(NOR5) clade	uncultured gamma proteobacterium
Proteobacteria	Gammaproteobacteria	Cellvibrionales	Haliaceae	OM60(NOR5) clade	uncultured <i>Glaciecola</i> sp.
Proteobacteria	Gammaproteobacteria	Cellvibrionales	Haliaceae	OM60(NOR5) clade	uncultured marine microorganism
Proteobacteria	Alphaproteobacteria	Thalassobaculales	Nisaeaceae	OM75 clade	uncultured alpha proteobacterium
Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	<i>Parablastomonas</i>	<i>Parablastomonas</i> sp.
Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Paracoccus</i>	<i>Paracoccus</i> sp.
Proteobacteria	Gammaproteobacteria	Cellvibrionales	Haliaceae	<i>Parahaliaea</i>	<i>Parahaliaea</i> sp.
Proteobacteria	Alphaproteobacteria	Caulobacteriales	Parvularculaceae	<i>Parvularcula</i>	<i>Parvularcula</i> sp.

<i>Phylum</i>	<i>Class</i>	<i>Order</i>	<i>Family</i>	<i>Genus</i>	<i>Species</i>
Proteobacteria	Alphaproteobacteria	Rhodovibrionales	Kiloniellaceae	<i>Pelagibius</i>	<i>Pelagibius</i> sp.
Proteobacteria	Deltaproteobacteria	Desulfuromonadales	Desulfuromonadaceae	<i>Pelobacter</i>	<i>Pelobacter</i> sp.
Proteobacteria	Deltaproteobacteria	Bdellovibrionales	Bacteriovoraceae	<i>Peredibacter</i>	<i>Peredibacter</i> sp.
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	<i>Perlucidibaca</i>	<i>Perlucidibaca piscinae</i>
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	<i>Perlucidibaca</i>	<i>Perlucidibaca</i> sp.
Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	<i>Photobacterium</i>	<i>Photobacterium damselae</i> subsp. <i>damselae</i> CIP 102761
Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	<i>Pseudahrensia</i>	<i>Pseudahrensia</i> sp. uncultured
Proteobacteria	Gammaproteobacteria	Alteromonadales	Pseudoalteromonadaceae	<i>Pseudoalteromonas</i>	<i>Pseudoalteromonas</i> sp.
Proteobacteria	Gammaproteobacteria	Oceanospirillales	Pseudohongiellaceae	<i>Pseudohongiella</i>	uncultured gamma proteobacterium
Proteobacteria	Gammaproteobacteria	Oceanospirillales	Pseudohongiellaceae	<i>Pseudohongiella</i>	uncultured <i>Marinomonas</i> sp.
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	<i>Pseudomonas</i>	<i>Pseudomonas</i> sp. enrichment culture clone SYW24
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	<i>Pseudomonas</i>	<i>Pseudomonas</i> sp.
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	<i>Psychrobacter</i>	<i>Psychrobacter</i> sp.
Proteobacteria	Alphaproteobacteria	Reyranellales	Reyranellaceae	<i>Reyranella</i>	<i>Reyranella</i> sp.
Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	<i>Rheinheimera</i>	<i>Rheinheimera</i> sp.
Proteobacteria	Alphaproteobacteria	Azospirillales	Azospirillaceae	<i>Rhodocista</i>	<i>Rhodospirillum</i> sp.
Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Rhodovulum</i>	<i>Rhodovulum</i> sp.
Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Ruegeria</i>	<i>Ruegeria</i> sp.
Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Salinhabitans</i>	<i>Salinhabitans</i> sp.
Proteobacteria	Deltaproteobacteria	Myxococcales	Sandaracinaceae	<i>Sandaracinus</i>	<i>Sandaracinus</i> sp.
Proteobacteria	Gammaproteobacteria	Chromatiales	Sedimenticolaceae	<i>Sedimenticola</i>	<i>elarraichensis</i> gill symbiont
Proteobacteria	Gammaproteobacteria	Alteromonadales	Shewanellaceae	<i>Shewanella</i>	<i>Shewanella</i> sp.
Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Shimia</i>	uncultured <i>Shimia</i> sp.
Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Silicimonas</i>	<i>Silicimonas</i> sp.
Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	<i>Sphingobium</i>	<i>Sphingobium</i> sp.
Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	<i>Sphingomonas</i>	<i>Sphingomonas</i> sp.
Proteobacteria	Gammaproteobacteria	Ectothiorhodospirales	Thioalkalispiraceae	SS1-B-09-64	uncultured bacterium
Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	<i>Stenotrophomonas</i>	uncultured <i>Stenotrophomonas</i> sp.
Proteobacteria	Deltaproteobacteria	Desulfobacterales	Desulfobacteraceae	Sva0081 sediment group	uncultured bacterium
Proteobacteria	Deltaproteobacteria	Desulfobacterales	Desulfobacteraceae	Sva0081 sediment group	uncultured delta proteobacterium
Proteobacteria	Deltaproteobacteria	Desulfobacterales	Desulfobacteraceae	Sva0081 sediment group	uncultured marine bacterium
Proteobacteria	Gammaproteobacteria	Nitrosococcales	Nitrosococcaceae	SZB85	uncultured bacterium
Proteobacteria	Alphaproteobacteria	Rhodospirillales	Terasakiellaceae	<i>Terasakiella</i>	<i>Terasakiella</i> sp.

<i>Phylum</i>	<i>Class</i>	<i>Order</i>	<i>Family</i>	<i>Genus</i>	<i>Species</i>
Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Thalassobius</i>	<i>Thalassobius</i> sp.
Proteobacteria	Alphaproteobacteria	Rhodospirillales	Thalassospiraceae	<i>Thalassospira</i>	<i>Thalassospira</i> sp.
Proteobacteria	Gammaproteobacteria	Ectothiorhodospirales	Ectothiorhodospiraceae	<i>Thiogranum</i>	<i>Thiogranum</i> sp.
Proteobacteria	Gammaproteobacteria	Chromatiales	Chromatiaceae	<i>Thiohalobacter</i>	<i>Thiohalobacter</i> sp.
Proteobacteria	Gammaproteobacteria	Chromatiales	Chromatiaceae	<i>Thiohalocapsa</i>	<i>Thiohalocapsa</i> sp.
Proteobacteria	Alphaproteobacteria	Rhodovibrionales	Kiloniellaceae	<i>Tistlia</i>	<i>Tistlia</i> sp.
Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Tropicimonas</i>	<i>Tropicimonas</i> sp.
Proteobacteria	Deltaproteobacteria	Myxococcales	Nannocystaceae	<i>Enhygromyxa</i>	<i>Enhygromyxa</i> sp.
Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	uncultured	Alteromonadaceae bacterium NB0094
Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	uncultured	bacterium 10RO2
Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	uncultured	drinking water bacterium M3
Proteobacteria	Deltaproteobacteria	Myxococcales	Sandaracinaceae	uncultured	metagenome
Proteobacteria	Alphaproteobacteria	Caulobacterales	Parvularculaceae	<i>Parvularcula</i>	<i>Parvularcula</i> sp.
Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	uncultured	<i>Sphingomonadaceae</i> bacterium BL116
Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	uncultured	uncultured alpha proteobacterium
Proteobacteria	Alphaproteobacteria	Rhodospirillales	Magnetospiraceae	uncultured	uncultured alpha proteobacterium
Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	uncultured	uncultured bacterium
Proteobacteria	Alphaproteobacteria	Rhodovibrionales	Kiloniellaceae	uncultured	uncultured bacterium
Proteobacteria	Gammaproteobacteria	Gammaproteobacteria	Unknown Family	uncultured	uncultured bacterium
Proteobacteria	Gammaproteobacteria	Incertae Sedis		uncultured	uncultured bacterium
Proteobacteria	Gammaproteobacteria	Thiotrichales	Thiotrichaceae	uncultured	uncultured bacterium
Proteobacteria	Alphaproteobacteria	Caulobacterales	Hyphomonadaceae	uncultured	uncultured bacterium
Proteobacteria	Deltaproteobacteria	Bdellovibrionales	Bacteriovoracaceae	uncultured	uncultured bacterium
Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	uncultured	uncultured bacterium
Proteobacteria	Deltaproteobacteria	Myxococcales	Sandaracinaceae	uncultured	uncultured bacterium
Proteobacteria	Deltaproteobacteria	Oligoflexales	Oligoflexaceae	uncultured	uncultured bacterium
Proteobacteria	Gammaproteobacteria	Ectothiorhodospirales	Ectothiorhodospiraceae	uncultured	uncultured bacterium
Proteobacteria	Alphaproteobacteria	Rhizobiales	Methyloligellaceae	uncultured	uncultured bacterium
Proteobacteria	Deltaproteobacteria	Desulfarculales	Desulfarculaceae	uncultured	uncultured bacterium
Proteobacteria	Deltaproteobacteria	Syntrophobacteriales	Syntrophobacteraceae	uncultured	uncultured bacterium
Proteobacteria	Deltaproteobacteria	Desulfobacterales	Desulfobulbaceae	uncultured	uncultured Desulfobulbaceae bacterium
Proteobacteria	Gammaproteobacteria	Thiotrichales	Thiotrichaceae	uncultured	uncultured gamma proteobacterium
Proteobacteria	Gammaproteobacteria	Oceanospirillales	Nitrincolaceae	uncultured	uncultured gamma proteobacterium
Proteobacteria	Gammaproteobacteria	Thiotrichales	Thiotrichaceae	uncultured	uncultured marine bacterium
Proteobacteria	Deltaproteobacteria	Bdellovibrionales	Bacteriovoracaceae	uncultured	uncultured marine bacterium

<i>Phylum</i>	<i>Class</i>	<i>Order</i>	<i>Family</i>	<i>Genus</i>	<i>Species</i>
Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	uncultured	uncultured marine bacterium
Proteobacteria	Deltaproteobacteria	Myxococcales	Sandaracinaceae	uncultured	uncultured Myxococcales bacterium
Proteobacteria	Alphaproteobacteria	Rhodospirillales	Magnetospiraceae	uncultured	uncultured organism
Proteobacteria	Alphaproteobacteria	Rickettsiales	Anaplasmataceae	uncultured	uncultured organism
Proteobacteria	Alphaproteobacteria	Micavibrionales	Micavibrionaceae	uncultured	uncultured organism
Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	uncultured	uncultured Rhodobacteraceae bacterium
Proteobacteria	Alphaproteobacteria	Puniceispirillales	SAR116 clade	uncultured alpha proteobacterium	NA
Proteobacteria	Alphaproteobacteria	Parvibaculales	PS1 clade	uncultured alpha proteobacterium	NA
Proteobacteria	Alphaproteobacteria	Puniceispirillales	SAR116 clade	uncultured bacterium	NA
Proteobacteria	Deltaproteobacteria	Oligoflexales	Oligoflexaceae	uncultured bacterium	NA
Proteobacteria	Deltaproteobacteria	Myxococcales	Blfdi19	uncultured bacterium	NA
Proteobacteria	Alphaproteobacteria	SAR11 clade	Clade II	uncultured bacterium	NA
Proteobacteria	Alphaproteobacteria	Parvibaculales	PS1 clade	uncultured bacterium	NA
Proteobacteria	Alphaproteobacteria	SAR11 clade	Clade IV	uncultured bacterium	NA
Proteobacteria	Deltaproteobacteria	Myxococcales	P3OB-42	uncultured bacterium	NA
Proteobacteria	Gammaproteobacteria	Oceanospirillales	Gven-F17	uncultured bacterium	NA
Proteobacteria	Alphaproteobacteria	Rhodospirillales	AEGEAN-169 marine group	uncultured bacterium	NA
Proteobacteria	Alphaproteobacteria	SAR11 clade	Clade III	uncultured bacterium	NA
Proteobacteria	Alphaproteobacteria	Rickettsiales	S25-593	uncultured bacterium	NA
Proteobacteria	Deltaproteobacteria	Myxococcales	BIrii41	uncultured bacterium	NA
Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	uncultured Burkholderiales bacterium	NA
Proteobacteria	Alphaproteobacteria	Rhodospirillales	AEGEAN-169 marine group	uncultured marine bacterium	NA
Proteobacteria	Alphaproteobacteria	SAR11 clade	Clade III	uncultured marine microorganism	NA

<i>Phylum</i>	<i>Class</i>	<i>Order</i>	<i>Family</i>	<i>Genus</i>	<i>Species</i>
Proteobacteria	Deltaproteobacteria	Myxococcales	P3OB-42	uncultured Sorangiineae bacterium	NA
Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	<i>Variovorax</i>	<i>Variovorax</i> sp.
Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	<i>Vibrio</i>	<i>Vibrio</i> sp.
Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	<i>Vibrio</i>	<i>Vibrio</i> sp.
Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	<i>Vibrio</i>	<i>Vibrio aerogenes</i>
Proteobacteria	Gammaproteobacteria	Vibrionales	Vibrionaceae	<i>Vibrio</i>	<i>Vibrio azureus</i>
Proteobacteria	Gammaproteobacteria	Steroidobacterales	Woeseiaceae	<i>Woeseia</i>	<i>Woeseia</i> sp.
Proteobacteria	Alphaproteobacteria	Rhizobiales	Xanthobacteraceae	<i>Xanthobacter</i>	<i>Xanthobacter</i> sp.
Spirochaetes	Spirochaetia	Spirochaetales	Spirochaetaceae	<i>Spirochaeta</i> 2	<i>Spirochaeta</i> 2 sp.
TA06	uncultured bacterium	NA	NA	NA	NA
Tenericutes	Mollicutes	Acholeplasmatales	Acholeplasmataceae	<i>Acholeplasma</i>	<i>Acholeplasma</i> sp.
Unassigned	Unassigned	Unassigned	Unassigned	Unassigned	Unassigned
Verrucomicrobia	Verrucomicrobiae	Opitutales	Puniceococcaceae	<i>Coralimargarita</i>	<i>Coralimargarita</i> sp.
Verrucomicrobia	Verrucomicrobiae	Pedosphaerales	Pedosphaeraceae	SCGC AAA164-E04	uncultured bacterium
WPS-2	marine metagenome	NA	NA	NA	NA
WS2	uncultured bacterium	NA	NA	NA	NA

**Discussion.** Understanding the health and output of these ecosystems depends on knowledge of bacterial populations in seaweed farming. Popular seaweed species *K. alvarezii* is frequently afflicted by ice-ice disease, which can seriously limit its productivity and development.

Cyanobacteria, including *Acrophormium* at Site 1 and *Cyanobium* at Site 2, were identified. These bacteria are notable for their photosynthetic abilities, which contribute to primary production in the ecosystem.

The presence of *Synechococcus* CC9902 in the cultivation region of *K. alvarezii* does not directly indicate a negative impact on the health of *K. alvarezii*. *Synechococcus* CC9902 is a dominant species in the phylum Cyanobacteria, which accounts for 54% of the total bacteria detected at Site 1 and 43% at Site 2. This dominance suggests that *Synechococcus* CC9902 is well-adapted to the environment and likely plays a significant role in the ecosystem, possibly contributing to nutrient cycling and photosynthetic activity (Kim et al 2018). While *Synechococcus* CC9902 itself does not appear to be directly harmful to *K. alvarezii*, the overall bacterial community and environmental conditions can influence the health of the seaweed. For example, changes in salinity, temperature, and light intensity can affect *K. alvarezii* growth and susceptibility to diseases like ice-ice disease (Arasamuthu & Edward 2018).

The ice-ice disease in *K. alvarezii* is known to be influenced by a combination of environmental stressors and opportunistic bacterial pathogens, such as *Vibrio* species. The presence of these pathogens, rather than *Synechococcus* CC9902, is more directly linked to the disease. The presence of *Vibrio* species, which are known to be associated with ice-ice disease in *K. alvarezii*, is noted in both sites. This suggests that these bacteria could play a role in the disease's etiology, although the exact mechanism and impact on the disease progression are not detailed in the provided information (Azizi et al 2018; Riyaz et al 2019).

*Vibrio* bacteria play a significant role in the development of ice-ice disease in *K. alvarezii* cultures. Some studies have identified *V. alginolyticus* as one of the primary bacteria causing ice-ice disease in *K. alvarezii*. Other *Vibrio* species, such as *Vibrio* sp. (P11), have also been implicated in the disease (Largo et al 1995; Tahiluddin & Terzi 2021).

The differences in bacterial composition between Site 1 (seabed) and Site 2 (depth 30-50 cm) provide insights into the ecological dynamics of *K. alvarezii* culture. For instance, Site 1 may suffer higher levels of organic matter breakdown due to the presence of additional Bacteroidetes species, such as *Actibacter* and *Aureicoccus*. Site 2 might feature a more diversified community with a higher presence of Actinobacteria such *Candidatus actinomarina* and *Gordonia*, indicating a larger range of metabolic activities.

**Conclusions.** By means of DNA metabarcoding, the bacterial composition at two separate sites within *K. alvarezii* culture locations has been thoroughly understood. Important responsibilities in decomposing organic matter, recycling nutrients, supporting primary production, and preserving ecosystem balance are played by the leading phyla—Cyanobacteria, and Proteobacteria. Ice-ice disease in *K. alvarezii* cultures is associated with particular bacterial species like *Vibrio* spp. and *Pseudoalteromonas* sp. Understanding the microbial dynamics involved will help properly manage and conserve *K. alvarezii* aquaculture systems.

**Acknowledgements.** The authors would like to thank University of Mataram for funding this research through the 2023 Research and Community Service Grant program. The authors also deeply appreciate the people of Labuhan Sangoro Village for helping the team in sampling activities and The Agency of Environmental Service of Sumbawa Regency, NTB for giving us much information regarding ice-ice disease outbreak.

**Conflict of Interest.** The authors declare that there is no conflict of interest.



## References

- Abdelfattah A., Malacrinò A., Wisniewski M., Cacciola S. O., Schena L., 2018 Metabarcoding: A powerful tool to investigate microbial communities and shape future plant protection strategies. *Biological Control* 120:1-10.
- Afianti N. F., Darmayati Y., 2019 [Culture independent approach to bacterial community analysis]. *Oseana* 42(1):9-17.
- Arasamuthu A., Edward J. K. P., 2018 Occurrence of ice-ice disease in seaweed *Kappaphycus alvarezii* at Gulf of Mannar and Palk Bay, Southeastern India. *Indian Journal of Geo-Marine Sciences* 47(6):1208-1216.
- Aris M., Labenua R., 2020 Horizontal transmission of ice-ice disease in seaweed *Kappaphycus alvarezii* (Doty) L. M. Liao (Gigartinales, Rhodophyta). *Hidrobiologica* 30(2):155-161.
- Aris M., Ibrahim A., Perairan S. B., Perikanan F., Kelautan D., Khairun U., 2020 [Transmission rate of ice-ice disease in *Kappaphycus alvarezii* seaweed based on planting distance using the longline method]. *Budidaya Perairan* 8(2):82-90. [In Indonesian].
- Arisandi A., Farid A., 2014 [Impact of ecological factors on the spread of ice-ice disease]. *Jurnal Kelautan: Indonesian Journal of Marine Science and Technology* 7(1):20-25. [In Indonesian].
- Asaf R., Athirah A., Paena M., 2021 [Optimizing the development of seaweed (*Kappaphycus alvarezii*) cultivation business in the waters of Kulisusu Bay, North Buton Regency, Southeast Sulawesi Province]. *Jurnal Sosial Ekonomi Kelautan Dan Perikanan* 16(1):39-50. [In Indonesian].
- Astria B. H., Cokrowati N., Putra A. P., 2023 [Analysis of pollution level of waters at seaweed farms location, Labuhan Sangoro, Saleh Bay, Sumbawa]. *Jurnal Perikanan* 13(3):744-754. [In Indonesian].
- Azis, Achmad M., Indarjo A., Salim G., Rozi, 2022 Identification of bacteria in seaweed (*Kappaphycus alvarezii*) affected by the ice-ice disease in Amal and Tanjung Tarakan waters, Indonesia. *AAFL Bioflux* 15(6):3061-3068.
- Azizi A., Hanafi N. M., Basiran M. N., Teo C. H., 2018 Evaluation of disease resistance and tolerance to elevated temperature stress of the selected tissue-cultured *Kappaphycus alvarezii* Doty 1985 under optimized laboratory conditions. *3 Biotech* 8(8):321.
- Callahan B. J., McMurdie P. J., Rosen M. J., Han A. W., Johnson A. J. A., Holmes S. P., 2016 DADA2: High-resolution sample inference from Illumina amplicon data. *Nature Methods* 13(7):581-583.
- Erbabley N. Y. G. F., Kelabora D. M., 2018 [Identification of seaweed bacteria *Kappaphycus alvarezii* based on growing season in Southeast Maluku waters]. *Akuatika Indonesia* 3(1):19. [In Indonesian].
- Kane S. N., Mishra A., Dutta A. K., 2016 Preface: International Conference on Recent Trends in Physics (ICRTP 2016). *Journal of Physics: Conference Series* 755(1).
- Kim Y., Jeon J., Kwak M. S., Kim G. H., Koh I. S., Rho M., 2018 Photosynthetic functions of *Synechococcus* in the ocean microbiomes of diverse salinity and seasons. *PLoS ONE* 13(1):e0190266.
- Largo D. B., Fukami K., Nishijima T., 1995 Occasional pathogenic bacteria promoting ice-ice disease in the carrageenan-producing red algae *Kappaphycus alvarezii* and *Eucheuma denticulatum* (Solieriaceae, Gigartinales, Rhodophyta). *Journal of Applied Phycology* 7(6):545-554.
- Pranata B., Kusuma A. B., Sabariah V., Kim H. W., Andriyono S., 2022 Environmental DNA metabarcoding reveals biodiversity marine fish diversity of a small island at Manokwari District, West Papua, Indonesia. *Biodiversitas* 23(11):5982-5988.
- Riyaz S. U. M., Nalini S., Kavitha G., Sutha S. A. D., Inbakandan D., 2019 Characterization and identification of isolated bacteria from ice-ice disease infected seaweed *Kappaphycus alvarezii*. *Indian Journal of Geo-Marine Sciences* 48(8):1286-1290.
- Rupert R., Rodrigues K. F., Thien V. Y., Yong W. T. L., 2022 Carrageenan from *Kappaphycus*

*alvarezii* (Rhodophyta, Solieriaceae): Metabolism, structure, production, and application. *Frontiers in Plant Science* 13:859635.

- Santoso L., Nugraha Y. T., 2008 [The controlling of ice-ice diseases to increase seaweeds production in Indonesia]. *Saintek Perikanan* 3(2):37-43. [In Indonesian].
- Tahiluddin A. B., Terzi E., 2021 Ice-ice disease in commercially cultivated seaweeds *Kappaphycus* spp. and *Eucheuma* spp.: A review on the causes, occurrence, and control measures. *Marine Science and Technology Bulletin* 10(3):234-243.
- Yilmaz P., Parfrey L. W., Yarza P., Gerken J., Pruesse E., Quast C., Schweer T., Peplies J., Ludwig W., Glöckner F. O., 2014 The SILVA and "all-species Living Tree Project (LTP)" taxonomic frameworks. *Nucleic Acids Research* 42(D1):643-648.
- Yulius, Heriati A., Mustikasari E., Zahara R. I., 2017 [Characteristics of tides and waves in the waters of Saleh Bay, West Nusa Tenggara]. *Jurnal Segara* 13(1):65-73. [In Indonesian].
- Zhou Z., Fang L., Meng Q., Li S., Chai S., Liu S., Schonewille J. T., 2017 Assessment of ruminal bacterial and archaeal community structure in yak (*Bos grunniens*). *Frontiers in Microbiology* 8:179.

Received: 13 September 2024. Accepted: 18 October 2024. Published online: 04 December 2024.

Authors:

Baiq Hilda Astriana, Marine Science Study Program, Faculty of Agriculture, University of Mataram, Jl. Pendidikan no. 37, 83125 Mataram, West Nusa Tenggara, Indonesia, e-mail: hilda.baiq@unram.ac.id

Edwin Jefri, Marine Science Study Program, Faculty of Agriculture, University of Mataram, Jl. Pendidikan No. 37, 83125 Mataram, West Nusa Tenggara, Indonesia, e-mail: ejefri@unram.ac.id

Mahardika Rizqi Himawan, Marine Science Study Program, Faculty of Agriculture, University of Mataram, Jl. Pendidikan No. 37, 83125 Mataram, West Nusa Tenggara, Indonesia, e-mail: mahardika@unram.ac.id

Lutfi Anggadhanita, Research Center for Applied Microbiology, National Research and Innovation Agency (BRIN), Jalan Raya Jakarta-Bogor Km 46, Soekarno Science Center, Cibinong, 16911 Bogor, West Java, Indonesia, e-mail: lutf009@brin.go.id

Aryan Perdana Putra, Master Program in Environmental Science, Muhammadiyah University of Mataram, Jl. KH Ahmad Dahlan No. 1, Pagesangan, 83125 Mataram, West Nusa Tenggara, Indonesia, e-mail: aya013@yahoo.co.id

Baiq Fadila Arlina, Environmental Science Study Program, Faculty of Mathematics and Natural Sciences, University of Mataram, Jl. Majapahit No. 62, 83125 Mataram, West Nusa Tenggara, Indonesia, e-mail: baiq.fadila02@gmail.com

This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution and reproduction in any medium, provided the original author and source are credited.

How to cite this article:

Astriana B. H., Jefri E., Himawan M. R., Anggadhanita L., Putra A. P., Arlina B. F., 2024 Using DNA metabarcoding to identify the bacteria composition in water at *Kappaphycus alvarezii* cultivation sites infected by ice-ice from Labuhan Sangoro, Sumbawa, Indonesia. *AAFL Bioflux* 17(6):2696-2717.